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ARAND et al

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For: EPOXIDE...ORIGIN



## SEQUENCE LISTING

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78

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 FURSTOSS, ROLAND

<120> EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN

<130> bml-410.018

<140> 10/009,030

<141> 2001-11-02

<150> PCT/FR00/01217

<151> 2000-05-05

<150> FR 99/05711

<151> 1999-05-05

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1197

<212> DNA

<213> Aspergillus niger

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<221> CDS

<222> (1)..(1194)

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aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96  
 Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys  
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acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144  
 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192  
 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240  
 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288  
 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca	336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala	
100 105 110	
ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
115 120 125	
cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg	432
Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
130 135 140	
gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
145 150 155 160	
gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
165 170 175	
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Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
180 185 190	
att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
195 200 205	
aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
210 215 220	
ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
225 230 235 240	
atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
245 250 255	
act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala	
260 265 270	
tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
275 280 285	
ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
290 295 300	
gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act	960
Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
305 310 315 320	

gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
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cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg 1056  
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cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
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cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152  
 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
                   370                                  375                                  380

aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197  
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<212> PRT

<213> Aspergillus niger

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                   20                                  25                                  30

Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
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Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
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Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
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Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
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 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190  
 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205  
 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220  
 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240  
 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser  
 245 250 255  
 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala  
 260 265 270  
 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro  
 275 280 285  
 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr  
 290 295 300  
 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
 305 310 315 320  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
 325 330 335  
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 340 345 350  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
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 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 6  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

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ttgaattccc tacttctgcc acac 24

<210> 7  
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<223> Description of Artificial Sequence: Primer

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<223> Description of Artificial Sequence: Synthetic  
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44

## SEQUENCE LISTING

&lt;110&gt; C.N.R.S.

5 <120> PROTEINS OF FUNGAL ORIGIN AND DERIVATIVES,  
PROCESSES FOR OBTAINING THEM, AND THEIR USES, IN  
PARTICULAR FOR THE PREPARATION OF ENANTIOMERICALLY  
PURE MOLECULES

10 &lt;130&gt; EPOXSL

&lt;140&gt;

&lt;141&gt;

15 &lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

20 &lt;211&gt; 1197

&lt;212&gt; DNA

&lt;213&gt; Aspergillus niger

&lt;220&gt;

25 &lt;221&gt; CDS

&lt;222&gt; (1)..(1197)

Nucleotide sequence SEQ ID NO : 1

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1 5 10 15

35 aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96  
Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys  
20 25 30

40 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144  
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
35 40 45

45 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192  
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
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cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240  
Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
65 70 75 80

50 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288  
Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
85 90 95

55 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336  
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
100 105 110

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Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
115 120 125

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	130 135 140	
5	gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
	Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
	145 150 155 160	
10	gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
	Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
	165 170 175	
15	atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat	576
	Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
	180 185 190	
20	att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
	Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
	195 200 205	
25	aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag gcc	672
	Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
	210 215 220	
30	ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
	Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
	225 230 235 240	
35	atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
	Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
	245 250 255	
40	act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
	Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala	
	260 265 270	
45	tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
	Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
	275 280 285	
50	ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
	Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
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55	gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act	960
	Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
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60	gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att	1008
	Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile	
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65	cac aag ccg ttt ggg ttc tcc ttc ttc ccc aag gac ctt tgt cct gtg	1056
	His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val	
	340 345 350	
70	cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat	1104
	Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp	
	355 360 365	

cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152  
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 370 375 380

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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

25 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

30 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

35 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

40 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
 130 135 140

45 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
 145 150 155 160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu  
 165 170 175

50 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205

55 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220

60 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240

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	Leu	Leu	Ala	Trp	Ile	Gly	Glu	Lys	Tyr	Leu	Gln	Trp	Val	Asp	Lys	Pro	
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	Glu	Ser	Phe	Pro	Arg	Ala	Ile	His	Thr	Tyr	Arg	Glu	Thr	Thr	Pro	Thr	
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20	His	Lys	Pro	Phe	Gly	Phe	Ser	Phe	Phe	Pro	Lys	Asp	Leu	Cys	Pro	Val	
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25	His	Ala	Glu	Gly	Gly	His	Phe	Ala	Ala	Leu	Glu	Arg	Pro	Arg	Glu	Leu	
		370					375					380					
	Lys	Thr	Asp	Leu	Thr	Ala	Phe	Val	Glu	Gln	Val	Trp	Gln	Lys			
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